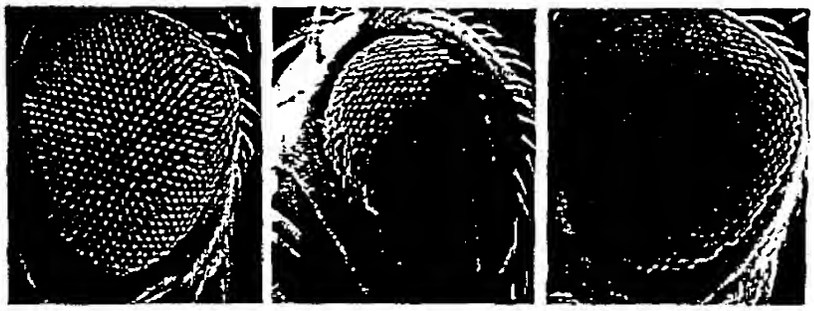
Figure 1

A



wild type | sev-wg | sev-wg, lgs^{S17}/+

B

C

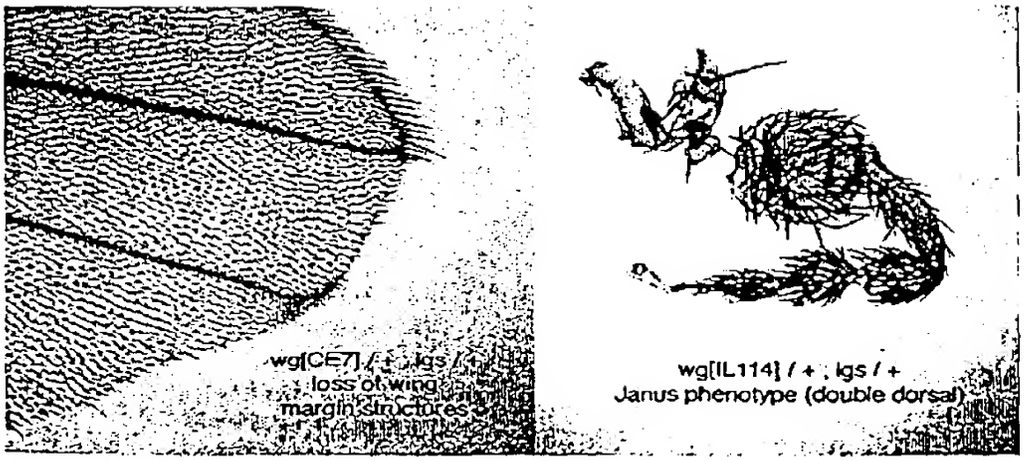


Figure 2

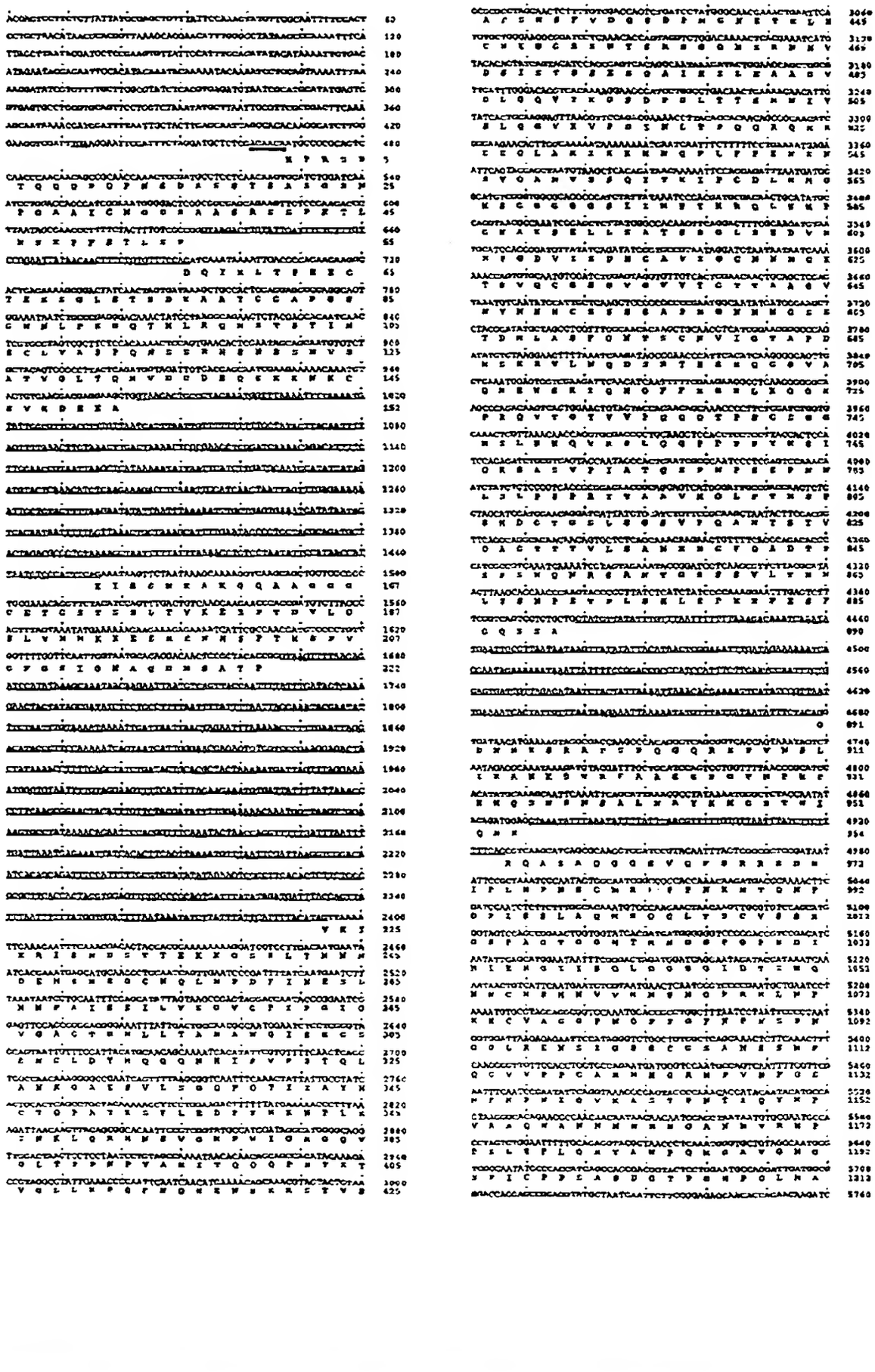
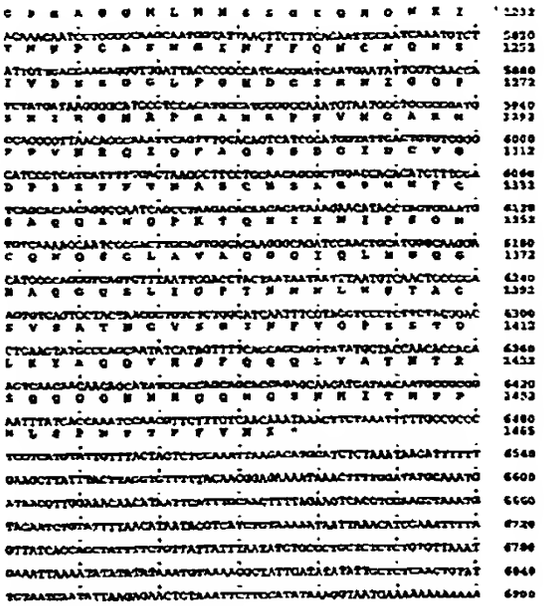


Figure 2: ***legless***



AAAAAAAAA 6909

Figure 3

A

yw x lgs anti-sense

yw x lgs sense

B

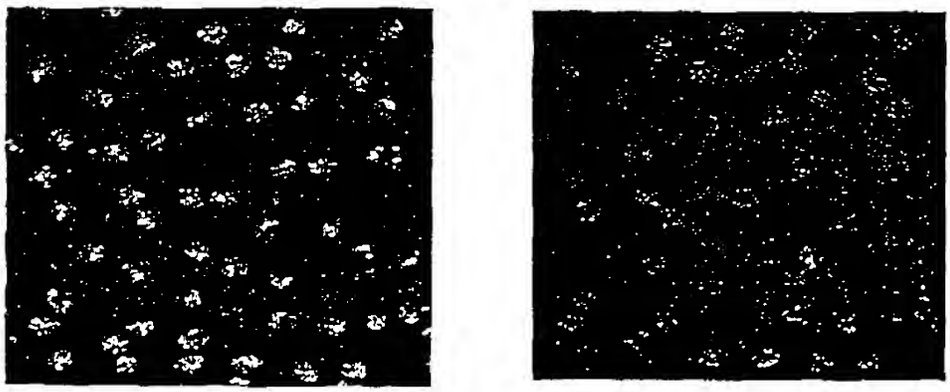


Figure 4

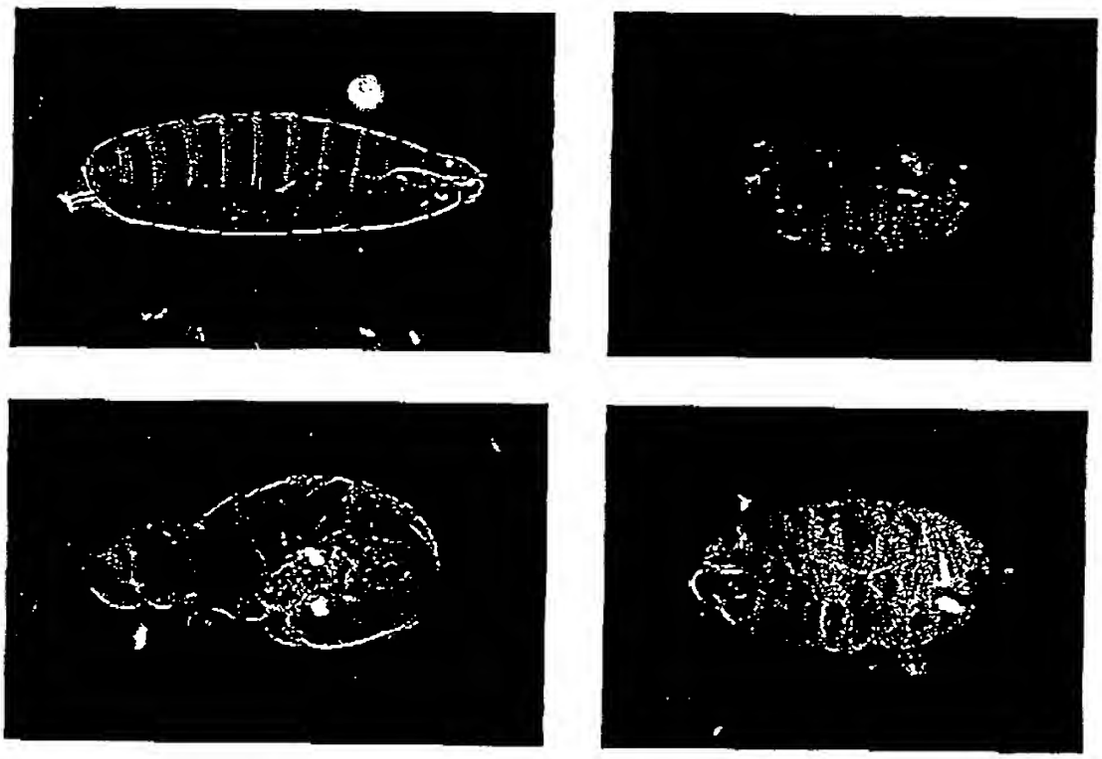
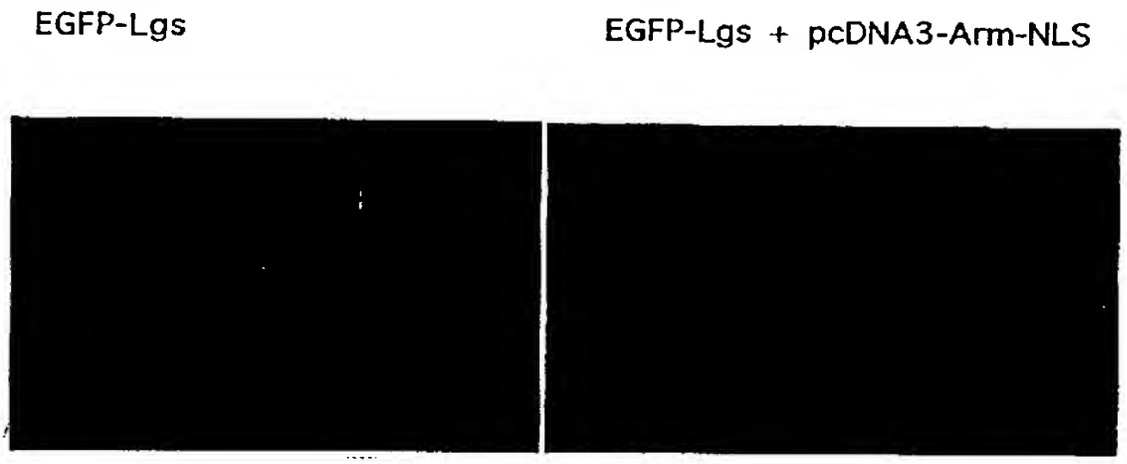
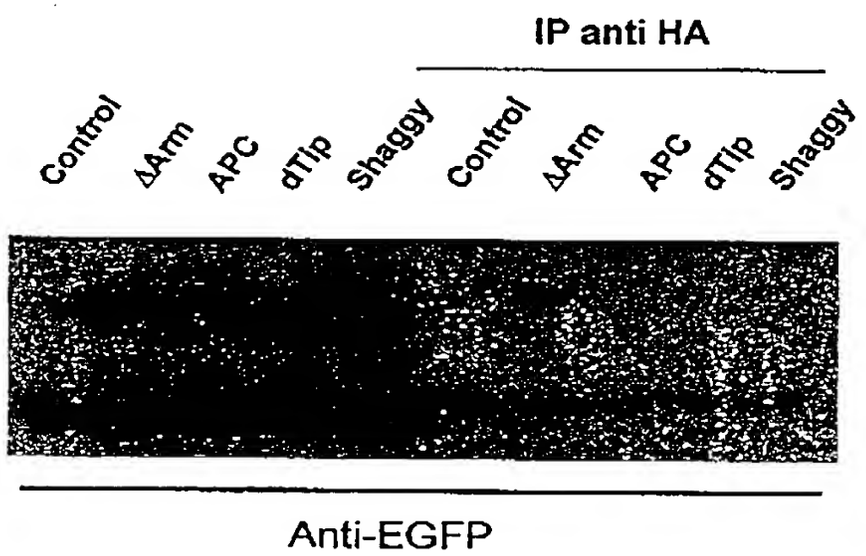


Figure 5

A


EGFP-Lgs
EGFP-Lgs + pcDNA3-Arm-NLS

B

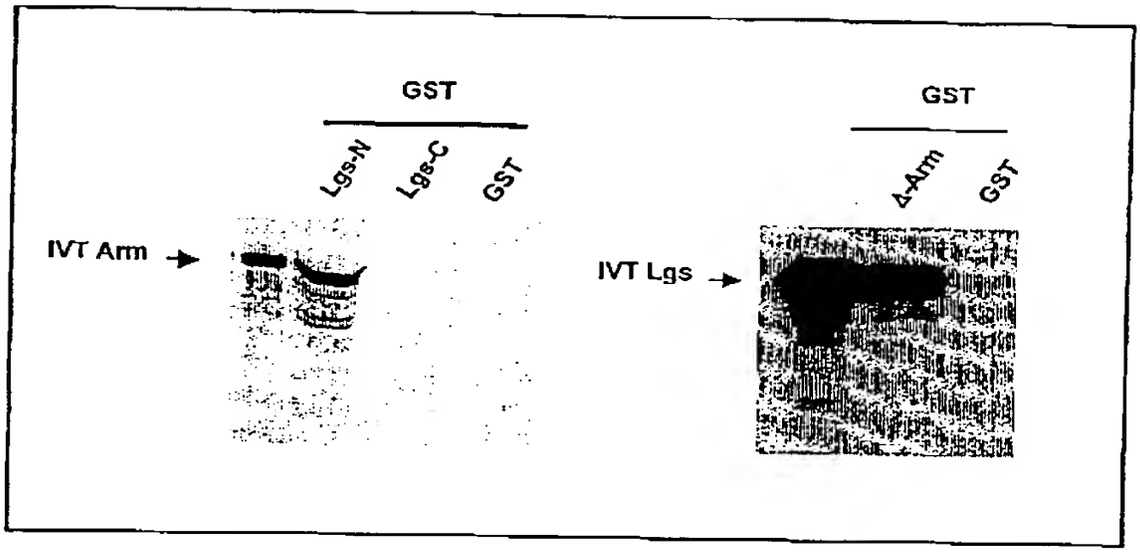

IP anti HA
Control
ΔArm
APC
dTip
Shaggy
Control
ΔArm
APC
dTip
Shaggy
Anti-EGFP

5C

		BAIT fusions: pLex						
		Lgs 1-1464	BCL9 199-392	BCL9 1-1426	Dco+	ΔArmC	Δß-Cat	Pan
PREY fusions: pJG4-5	lgs364-555							
	lgs1-385							
	lgs1-732							
	lgs364-1090							
	lgs726-1464							
	lgs1-1464							
	BCL9 199-392						n.d.	
	BCL91-1426							
	Dco+							
	DAxin							
	ΔArmC							
	ß-Cat							
	Pan							
	pJG4-5							

+: interaction seen in yeast two-hybrid assay
-: no interaction seen in yeast two-hybrid assay
n.d.: not done
numberings refer to amino acid positions.

5 D


GST
Lgs-N
Lgs-C
GST
IVT Arm
GST
Δ-Arm
GST
IVT Lgs

5 E

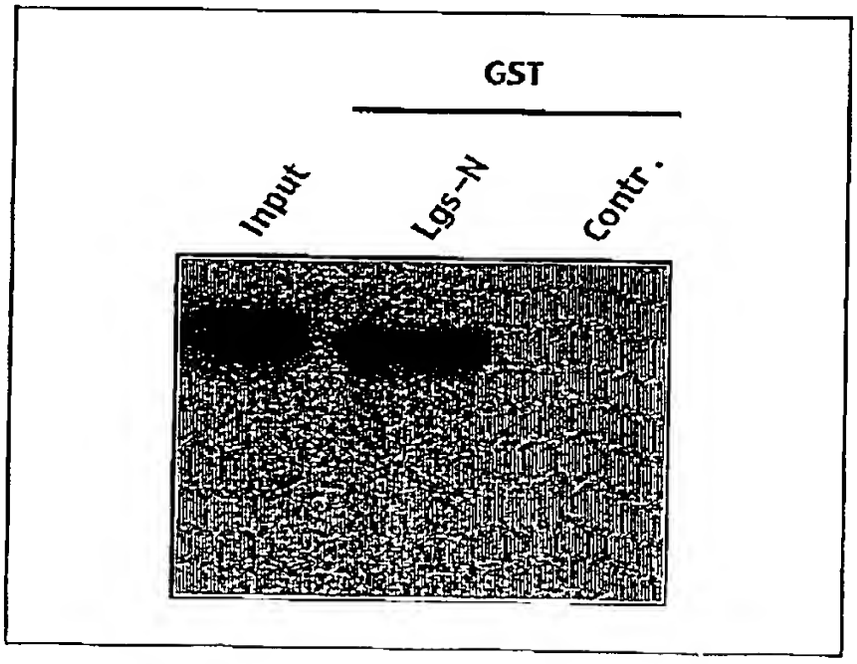

GST
Input
Lgs-N
Contr.

Figure 6

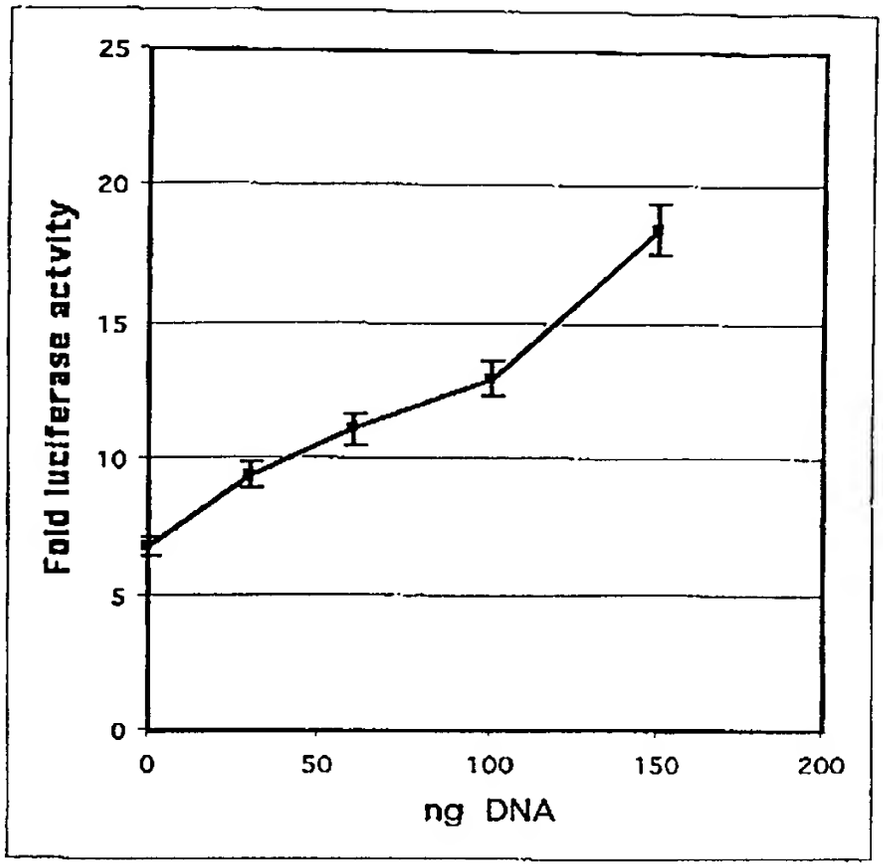
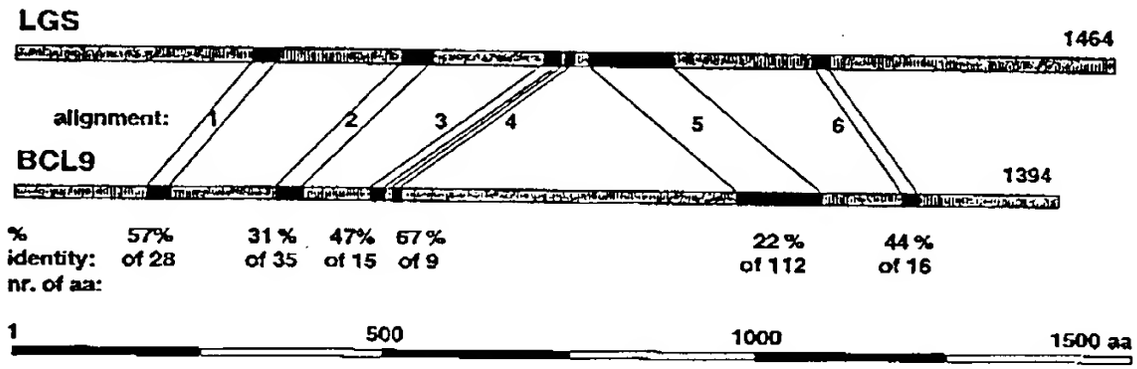


Figure 7

A


LGS
1464
alignment:
1
2
3
4
5
6
BCL9
1394
% identity:
nr. of aa:
57% of 28
31 % of 35
47% of 15
67 % of 9
22 % of 112
44 % of 16
1
500
1000
1500 aa

7B

Sequence homology domain 1: 57.1% identity in 28 aa

```
        320        330        340
LGS     IFVFSTQLANKGAESVLSGQFQTIIAYH
        ..:::::.:::.::.:: :: .:::...:
BCL9    VYVFSTEMANKAAEAVLKGQVETIVSFH
         180        190        200
```

Sequence homology domain 2: 31.4% identity in 35 aa

```
          520        530        540
LGS     ENLTPQQRQHREEQLAKIKKMNQFLFPENENSVGA
        ..:...: .:::  :  .. ... :::.. . .::
BCL9    DGLSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGA
       350        360        370        380
```

Sequence homology domain 3: 46.7% identity in 15 aa

```
          710        720
LGS     QMEWSKIQHQFFEER
        :..: :.:..:.::.
BCL9    QIANLKLQQEFYEEK
       470        480
```

Sequence homology domain 4: 66.6% identity in 9 aa

```
           760
LGS     LQGPPPPYH
        ..:::::::.
BCL9    VRGPPPPYQ
              520
```

Sequence homology domain 5: 22.3% identity in 112 aa

```
        770        780        790        800        810        820
LGS     SASVPIATQSPNPSSPNNLSLPSPRTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQA
        ... :.:.:... . :..:. ..: : ..   :. :. :.   . .:  . ...:.  ..
BCL9    GPPPPTASQPASVNIPGSLPSSTPYTMPPEPTLSQNPLSIM-MSRMSKFAMPSSTPLYHD
       970        980        990       1000       1010       1020

        830        840        850        860        870
LGS     GTTTVLSANRNCFQADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSP
        .. :: :.. .  .: .:. .. :   . : ..   .  ..:: .:.. :::
BCL9    AIKTVASSDDDSPPARSPNLPSMNNMPGMGINTQNPRISGPNPVVPMPTLSP
       1030       1040       1050       1060       1070
```

Sequence homology domain 6: 43.8% identity in 16 aa

```
           1080
LGS     NPRMCVAGGPNGPPGF
        .. .: .:::.:: .:

BCL9    DAALCKPGGPGGPDSF
      1190       1200
```

Figure 8

A

ATGCATTCCAGTAACCCTAAAGTGAGGAGCTCTCCATCAGGAAACACACA
GAGTAGCCCTAAGTCAAAGCAGGAGGTGATGGTCCGTCCCCCTACAGTGA
TGTCCCCATCTGGAAACCCCCAGCTGGATTCCAAATTCTCCAATCAGGGT
AAACAGGGGGGCTCAGCCAGCCAATCCCAGCCATCCCCCTGTGACTCCAA
GAGTGGGGGCCATACCCCTAAAGCACTCCCTGGCCCAGGTGGGAGCATGG
GGCTGAAGAATGGGGCTGGAAATGGTGCCAAGGGCAAGGGGAAAAGGGAG
CGAAGTATTTCCGCCGACTCCTTTGATCAGAGAGATCCTGGGACTCCAAA
CGATGACTCTGACATTAAAGAATGTAATTCTGCTGACCACATAAAGTCCC
AGGATTCCCAGCACACACCACACTCGATGACCCCATCAAATGCTACAGCC
CCCAGGTCTTCTACCCCCTCCCATGGCCAAACTACTGCCACAGAGCCCAC
ACCTGCTCAGAAGACTCCAGCCAAAGTGGTGTACGTGTTTTCTACTGAGA
TGGCCAATAAAGCTGCAGAAGCTGTTTTGAAGGGCCAGGTTGAAACTATC
GTCTCTTTCCACATCCAGAACATTTCTAACAACAAGACAGAGAGAAGCAC
AGCGCCTCTGAACACACAGATATCTGCCCTTCGGAATGATCCGAAACCTC
TCCCACAACAGCCCCCAGCTCCGGCCAACCAGGACCAGAATTCTTCCCAG
AATACCAGACTGCAGCCAACTCCACCCATTCCGGCACCAGCACCCAAGCC
TGCCGCACCCCCACGTCCCCTGGACCGGGAGAGTCCTGGGGTAGAAAACA
AACTGATTCCTTCTGTAGGAAGTCCTGCCAGCTCCACTCCACTGCCCCCA
GATGGTACTGGGCCCAACTCAACTCCCAACAATAGGGCAGTGACCCCTGT
CTCCCAGGGGAGCAATAGCTCTTCAGCAGATCCCAAAGCCCCTCCGCCTC
CACCAGTGTCCAGTGGCGAGCCCCCCACACTGGGAGAGAATCCCGATGGC
CTATCTCAGGAGCAGCTGGAGCACCGGGAGCGCTCCTTACAAACTCTCAG
AGATATCCAGCGCATGCTTTTTCCTGATGAGAAAGAATTCACAGGAGCAC
AAAGTGGGGGACCGCAGCAGAATCCTGGGGTATTAGATGGGCCTCAGAAA
AAACCAGAAGGGCCAATACAGGCCATGATGGCCCAATCCCAAAGCCTAGG
TAAGGGACCTGGGCCCCCGGACAGACGTGGGAGCTCCATTTGGCCCTCAAG
GACATAGAGATGTACCCTTTTCTCCAGATGAAATGGTTCCACCTTCTATG
AACTCCCAGTCTGGGACCATAGGACCCGACCACCTTGACCATATGACTCC
CGAGCAGATAGCGTGGCTGAAACTGCAGCAGGAGTTTTATGAAGAGAAGA
GGAGGAAGCAGGAACAAGTGGTTGTCCAGCAGTGTTCCCTCCAGGACATG
ATGGTCCATCAGCACGGGCCTCGGGGAGTGGTCCGAGGACCCCCCCCTCC
ATACCAGATGACCCCTAGTGAAGGCTGGGCACCTGGGGGTACAGAGCCAT
TTTCTGATGGTATCAACATGCCACATTCTCTGCCCCCGAGGGGCATGGCT
CCCCACCCCAACATGCCAGGGAGCCAGATGCGCCTCCCTGGATTTGCAGG
CATGATAAACTCTGAAATGGAAGGGCCGAATGTCCCCAACCCTGCATCTA
GACCAGGTCTTTCTGGAGTCAGTTGGCCAGATGATGTGCCAAAAATCCCA
GATGGTCGAAATTTTCCTCCTGGCCAGGGCATTTTCAGCGGTCCTGGCCG
AGGGGAACGCTTCCCAAACCCCCAAGGATTGTCTGAAGAGATGTTTCAGC
AGCAGCTGGCAGAGAAACAGCTGGGTCTCCCCCCAGGGATGGCCATGGAA
GGCATCAGGCCCAGCATGGAGATGAACAGGATGATTCCAGGCTCCCAGCG
CCACATGGAGCCTGGGAATAACCCCATTTTCCCTCGAATACCAGTTGAGG
GCCCTCTGAGTCCTTCTAGGGGTGACTTTCCAAAAGGAATTCCCCCACAG

Figure 8A

ATGGGCCCTGGTCGGGAACTTGAGTTTGGGATGGTTCCTAGTGGGATGAA
GGGAGATGTCAATCTAAATGTCAACATGGGATCCAACTCTCAGATGATAC
CTCAGAAGATGAGAGAGGCTGGGGCGGGCCCTGAGGAGATGCTGAAATTA
CGCCCAGGTGGCTCAGACATGCTGCCTGCTCAGCAGAAGATGGTGCCACT
GCCATTTGGTGAGCACCCCCAGCAGGAGTATGGCATGGGCCCCAGACCAT
TCCTTCCCATGTCTCAGGGTCCAGGCAGCAACAGTGGCTTGCGGAATCTC
AGAGAACCAATTGGGCCCGACCAGAGGACTAACAGCCGGCTCAGTCATAT
GCCACCACTACCTCTCAACCCTTCCAGTAACCCCACCAGCCTCAACACAG
CTCCTCCAGTTCAGCGCGGCCTGGGGCGGAAGCCCTTGGATATATCTGTG
GCAGGCAGCCAGGTGCATTCCCCAGGCATTAACCCTCTGAAGTCTCCCAC
GATGCACCAAGTCCAGTCACCAATGCTGGGCTCGCCCTCGGGGAACCTCA
AGTCCCCCCAGACTCCATCGCAGCTGGCAGGCATGCTGGCGGGCCCAGCT
GCTGCTGCTTCCATTAAGTCCCCCCCTGTTTTGGGGTCTGCTGCTGCTTC
ACCTGTCCACCTCAAGTCTCCATCACTTCCTGCCCCGTCACCTGGATGGA
CCTCTTCTCCAAAACCTCCCCTTCAGAGTCCTGGGATCCCTCCAAACCAT
AAAGCACCCCTCACCATGGCCTCCCCAGCCATGCTGGGAAATGTAGAGTC
AGGTGGCCCCCCACCTCCTACAGCCAGCCAGCCTGCCTCTGTGAATATCC
CTGGAAGTCTTCCCTCTAGTACACCTTATACCATGCCTCCAGAGCCAACC
CTTTCCCAGAACCCACTCTCTATTATGATGTCTCGAATGTCCAAGTTTGC
AATGCCCAGTTCCACCCCGTTATACCATGATGCTATCAAGACTGTGGCCA
GCTCAGATGACGACTCCCCTCCAGCTCGTTCTCCCAACTTGCCATCAATG
AATAATATGCCAGGAATGGGCATTAATACACAGAATCCTCGAATTTCAGG
TCCAAACCCCCGTGGTTCCGATGCCAACCCTCAGCCCAATGGGAATGACCC
AGCCACTTTCTCACTCCAATCAGATGCCCTCTCCAAATGCCGTGGGACCC
AACATACCTCCTCATGGGGTCCCAATGGGGCCTGGCTTGATGTCACACAA
TCCTATCATGGGGCATGGGTCCCAGGAGCCACCGATGGTACCTCAAGGAC
GGATGGGCTTCCCCCAGGGCTTCCCTCCAGTACAGTCTCCCCCACAGCAG
GTTCCATTCCCTCACAATGGCCCCAGTGGGGGGCAGGGCAGCTTCCCAGG
AGGGATGGGTTTCCCAGGAGAAGGCCCCCTTGGCCGCCCCAGCAACCTGC
CCCAAAGTTCAGCAGATGCAGCACTTTGCAAGCCTGGAGGCCCCGGGGGT
CCTGACTCCTTCACTGTCCTGGGGAACAGCATGCCTTCGGTGTTTACAGA
CCCAGATCTGCAGGAGGTCATCCGACCTGGAGCCACCGGAATACCTGAGT
TTGATCTATCCCGCATTATTCCATCTGAGAAGCCCAGCCAGACGCTGCAA
TATTTCCCTCGAGGGGAAGTTCCAGGCCGTAAACAGCCCCAGGGTCCTGG
ACCTGGGTTTTCACACATGCAGGGGATGATGGGCGAACAAGCCCCCAGAA
TGGGACTAGCATTACCTGGCATGGGAGGTCCAGGGCCAGTGGGAACTCCG
GACATCCCTCTTGGTACAGCTCCATCCATGCCAGGCCACAACCCCATGAG
ACCACCAGCCTTTCTCCAACAAGGCATGATGGGACCTCACCATCGGATGA
TGTCACCAGCACAATCTACAATGCCCCGGCCAGCCCACCCTGATGAGCAAT
CCAGCTGCTGCCGTGGGCATGATTCCTGGCAAGGATCGGGGGCCTGCCGG
GCTCTACACCCACCCTGGGCCTGTGGGCTCTCCAGGCATGATGATGTCCA
TGCAGGGCATGATGGGACCCCAACAGAACATCATGATCCCCCCACAGATG
AGGCCCCGGGGGCATGGCTGCTGACGTGGGCATGGGTGGATTTAGCCAAGG
ACCTGGCAACCCCAGGAAACATGATGTTTTAA

Figure 8B

B

MHSSNPKVRSSPSGNTQSSPKSKQEVMVRPPTVMSPSGNPQLDSKFSNQG
KQGGSASQSQPSPCDSKSGGHTPKALPGPGGSMGLKNGAGNGAKGKGKRE
RSISADSFDQRDPGTPNDDSDIKECNSADHIKSQDSQHTPHSMTPSNATA
PRSSTPSHGQTTATEPTPAQKTPAKVVYVFSTEMANKAAEAVLKGQVETI
VSFHIQNISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQ
NTRLQPTPPIPAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPP
DGTGPNSTPNNRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTLGENPDG
LSQEQLEHRERSLQTLRDIQRMLFPDEKEFTGAQSGGPQQNPGVLDGPQK
KPEGPIQAMMAQSQSLGKGPGPRTDVGAPFGPQGHRDVPFSPDEMPPPSM
NSQSGTIGPDHLDHMTPEQIAWLKLQQEFYEEKRRKQEQVVVQQCSLQDM
MVHQHGPRGVVRGPPPPYQMTPSEGWAPGGTEPFSDGINMPHSLPPRGMA
PHPNMPGSQMRLPGFAGMINSEMEGPNVPNPASRPGLSGVSWPDDVPKIP
DGRNFPPGQGIFSGPGRGERFPNPQGLSEEMFQQQLAEKQLGLPPGMAME
GIRPSMEMNRMIPGSQRHMEPGNINPIFPRIPVEGPLSPSRGDFPKGIPPQ
MGPGRELEFGMVPSGMKGDVNLNVNMGSNSQMIPQKMREAGAGPEEMLKL
PPGGSDMLPAQQKMVPLPFGEHPQQEYGMGPRPFLPMSQGPGSNSGLRNL
REPIGPDQRTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRGLGRKPLDISV
AGSQVHSPGINPLKSPTMHQVQSPMLGSPSGNLKSPQTPSQLAGMLAGPA
AAASIKSPPVLGSAAASPVHLKSPSLPAPSPGWTSSPKPPLQSPGIPPNH
KAPLTMASPAMLGNVESGGPPPPTASQPASVNIPGSLPSSTPYTMPPEPT
LSQNPLSIMMSRMSKFAMPSSTPLYHDAIKTVASSDDDSPPARSPNLPSM
NNMPGMGINTQNPRISGPNPVVPMPTLSPMGMTQPLSHSNQMPSPNAVGP
NIPPHGVPMGPGLMSHNPIMGHGSQEPPMVPQGRMGFPQGFPPVQSPPQQ
VPFPHNGPSGGQGSFPGGMGFPGEGPLGRPSNLPQSSADAALCKPGGPGG
PDSFTVLGNSMPSVFTDPDLQEVIRPGATGIPEFDLSRIIPSEKPSQTLQ
YFPRGEVPGRKQPQGPGPGFSHMQGMMGEQAPPMGLALPGMGGPGPVGTP
DIPLGTAPSMPGHNPMRPPAFLQQGMMGPHHRMMSPAQSTMPGQPTLMSN
PAAAVGMIPGKDRGPAGLYTHPGPVGSPGMMMSMQGMMGPQQNIMIPPQM
RPRGMAADVGMGGFSQGPGNPGNMMF*

Figure 9

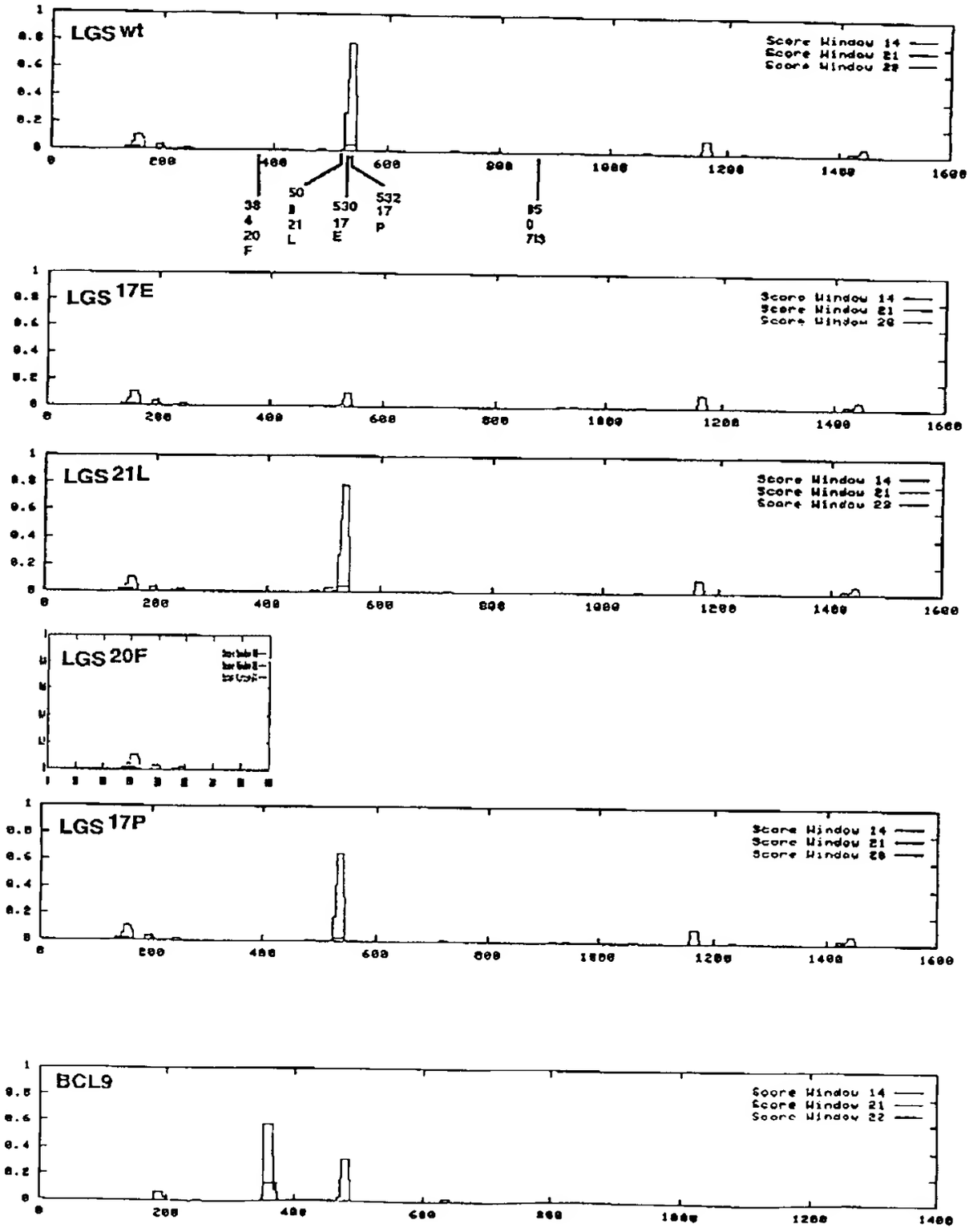

LGS wt
Score Window 14
Score Window 21
Score Window 22
38
4
20
F
50
8
21
L
530
17
E
532
17
P
85
0
715
LGS 17E
LGS 21L
LGS 20F
LGS 17P
BCL9

Figure 10

A

ATGGCCTGCTTCCCATCCCCTGCTGCCATCTCCTGCACCCTTAGGGCACAGTGGGCATCT
CGGGAGCTGCTCAGCGGACAGACTAGGGTTACCCCCACCCCAGGAGGAGAGAAGCTCCAG
GGAGCCCGCCGCTGTCCCCCGCGGTCATTGCCCCCTGCCCCAGCCAAGCCAATGCACCCA
GAAAATAAATTGACCAATCATGGCAAGACAGGGAATGGCGGGGCCCAATCTCAGCACCAG
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GGGGCCAAGGCCAACCAGATCTCGCCTAGCAACTCAAGTCTGAAGAACCCCCAGGCAGGG
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ATGATACAGAGGCTGGGCCAGGACAGCCTCACGCCTGAGCAGGTGGCCTGGCGCAAGCTG
CAGGAGGAGTACTACGAAGAGAAACGGCGGAAAGAGGAACAGATTGGGCTGCATGGGAGC
CGTCCTCTGCAGGACATGATGGGCATGGGGGGCATGATGGTGAGGGGGCCCCCGCCTCCT
TACCACAGCAAGCCTGGGGATCAGTGGCCACCTGGAATGGGTGCGCAGCTGCGGGGGCCC
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CCCCCTATGGGGGGACCCAGCAATTTTGCCCAGAACACCATGCCCTACCCAGGTGGGCAG
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CTGGAGAAGCGGTCGATGGGCATGCAGCGCCCCCTGGGCATGGCAGGCAGTGGCATGGGA
CAGAGCATGGAGATGGAGCGGATGATGCAGGCGCACCGACAGATGGATCCTGCCATGTTT
CCCGGGCAGATGGCTGGTGGTGAGGGCCTGGCGGGCACTCCCATGGGCATGGAGTTTGGT
GGAGGCCGGGGCCTCCTGAGCCCTCCCATGGGGCAGTCTGGGCTGAGGGAGGTGGACCCA
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CTGAACGTGCAGATGACCCCGCAGCAGCAGATGCTGATGTCGCAGAAGATGCGGGGCCCT
GGGGACTTGATGGGGCCCCAGGGCCTCAGTCCTGAGGAGATGGCCCGGGTTCGGGCCCAG
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CAGGGCTCCGGGCCAGGTGGCCCCGACTCCCTGAATGCCCCCTGTGGCCCAGTGCCCAGC
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CTGCAGAACATGATGGCGGAGCAGACTCCCTCTCGGCCTCCCAACCTCCCAGGCCAGCAG
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CAGCGGCAGCTGAAGGAGGCTTTGGAGAGGCTCCTGCCCCAGGTGGAGGCGGCCCGCAAG
GCCATCCGCGCCGCTCAGGTGGAGCGCTATGTGCCCGAACACGAGCGATGCTGCTGGTGC
CTGTGCTGCGGCTGTGAGGTGCGGGAACACCTGAGCCATGGAAACCTGACGGTGCTGTAC

Figure 10

GGGGGGCTGCTGGAGCATCTGGCCAGCCCAGAGCACAAGAAAGCAACCAACAAATTCTGG
TGGGAGAACAAAGCTGAGGTCCAGATGAAAGAGAAGTTTCTGGTCACTCCCCAGGATTAT
GCGCGATTCAAGAAATCCATGGTGAAAGGTTTGGATTCCTATGAAGAAAAGGAGGATAAA
GTGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAGCCGACAGGAGGTGGTT
CGGTCTGTCTTAGAGACAGGTCCCCCAAGATACGCCCTCACAGTCCGGTCCCCCGCCGTC
CTCTCCCGGCGCACGCTCAAGTCCGGTGCCTTCCCCCCGCAGACCCCCGAGGCGCACCCT
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GCAGGCAAAGCTAGAAAAACTGCGCTGCATTTGCAAACAAAAGCTCTTGTTGGCGATGAC
GATACTGTTTTGGGTGTGAAACTGTCAATTGCTAACTACGATCTGTGA

B

FKEDGFQDKASHFFSSTYSPETSRRKLPQAPKASFLGQQGRVIWKPLSEE
LRDQGADAAGGPASIMSPIATVNASGLSKEQLEHIRERSLQTLRDIERLLL
RSGETEPFLKGAPRRSGGLKKYEEPLQSMISQTQSLGGPPLEHEVPGHPP
GGDMGQQMNMMIQRLGQDSLTPEQVAWRKLQEEYYEEKRRKEEQIGLHGS
RPLQDMMGMGGMMMVRGPPPPYHSKPGDQWPPGMGAQLRGPMDVQDPMQLR
GGPPFPGPRFPGNQIQRVPGFGGMQSMPMEVPMNAMQRPVRPGMGWTEDL
PPMGGPSNFAQNTMPYPGGQGEAERFMTPRVREELLRHQLLEKRSMGMQR
PLGMAGSGMGQSMEMERMMQAHRQMDPAMFPGQMAGGEGLAGTPMGMEFG
GGRGLLSPPMGQSGLREVDPPMGPGNLNMNMNVNMNMNMNLNVQMTPQQQ
MLMSQKMRGPGDLMGPQGLSPEEMARVRAQNSSGMVPLPSANPPGPLKSP
QVLGSSLSVRSPTGSPSRLKSPSMAVPSPGWVASPKTAMPSPGVSQNKQP
PLNMNSSTTLSNMEQDPTPSQNPLSLMMTQMSKYAMPSSTPLYHNAIKTI
ATSDDELLPDRPLLPPPPPPQGSGPGGPDSLNAPCGPVPSSSQMMPFPPR
LQQPHGAMAPTGGGGGGPGLQQHYPSGMALPPEDLPNQPPGPMPPQQHLM
GKAMAGRMGDAYPPGVLPGVASVLNDPELSEVIRPTPTGIPEFDLSRIIP
SEKPSSTLQYFPKSENQPPKAQPPNLHLMNLQNMMAEQTPSRPPNLPGQQ
GDRPLVVVIPGTRAMAPAQRCPLCRQTFFCGRGHVYSRKHQRQLKEALER
LLPQVEAARKAIRAAQVERYVPEHERCCWCLCCGCEVREHILSHGNLTVLY
GGLLEHLASPEHKKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKG
LDSYEEKEDKVIKEMAAQIREVEQSRQEVVRSVLETGPPRYALTVRSPAV
LSRRTLKSGAFPPQTPEAHPQARCLCAPRRGALKPEPPGRTLKLGVPPHT
TRKARPHAAKTSPRPRCTRQAPNKTQSLQLAGKARKTALHLQTKALVGDD
DTVLGVKLSIANYDL

Figure 11

A

B

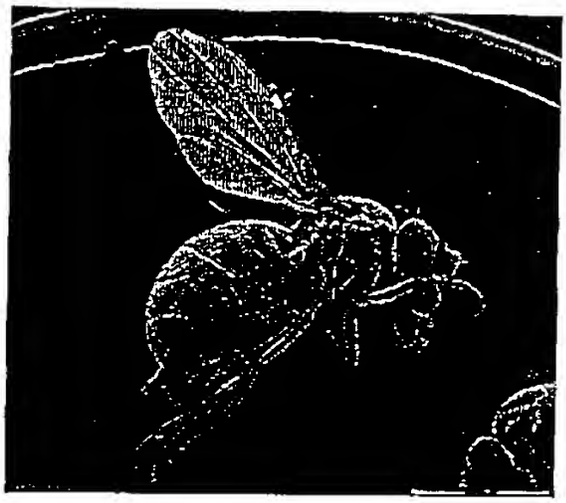
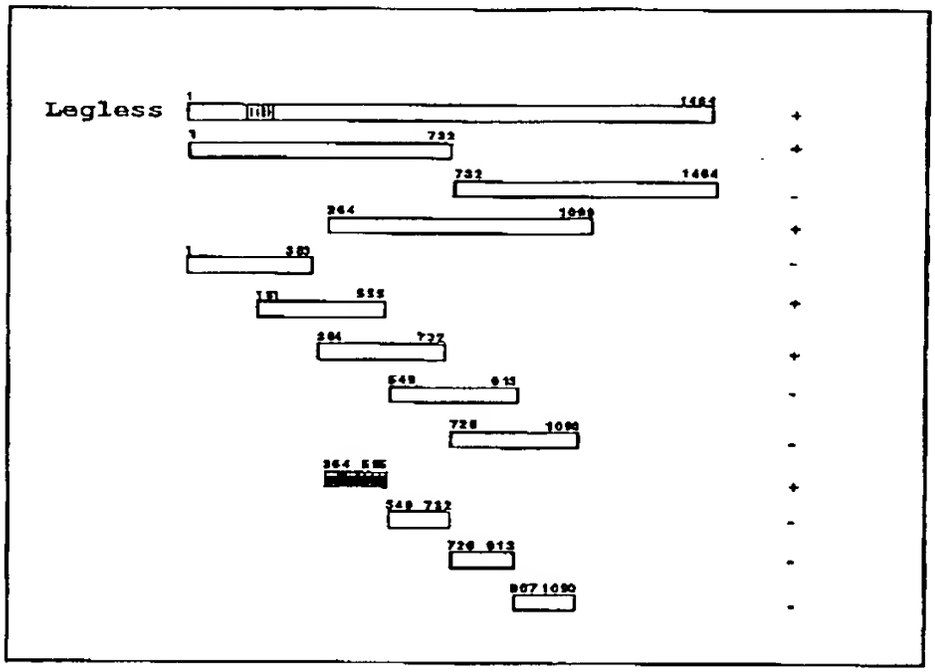


Figure 12

A


Legless
1
1464
1
732
732
1464
364
1090
1
383
181
555
364
732
549
913
728
1090
364
549
732
728
913
907
1090
+
+
-
+
-
+
+
-
-
+
-
-
-

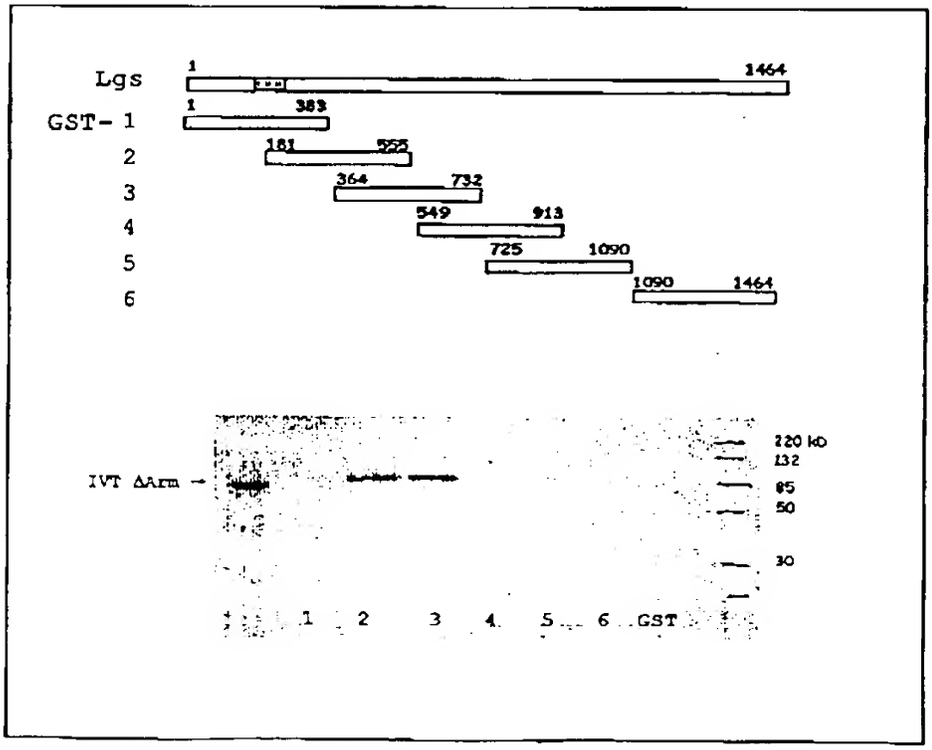
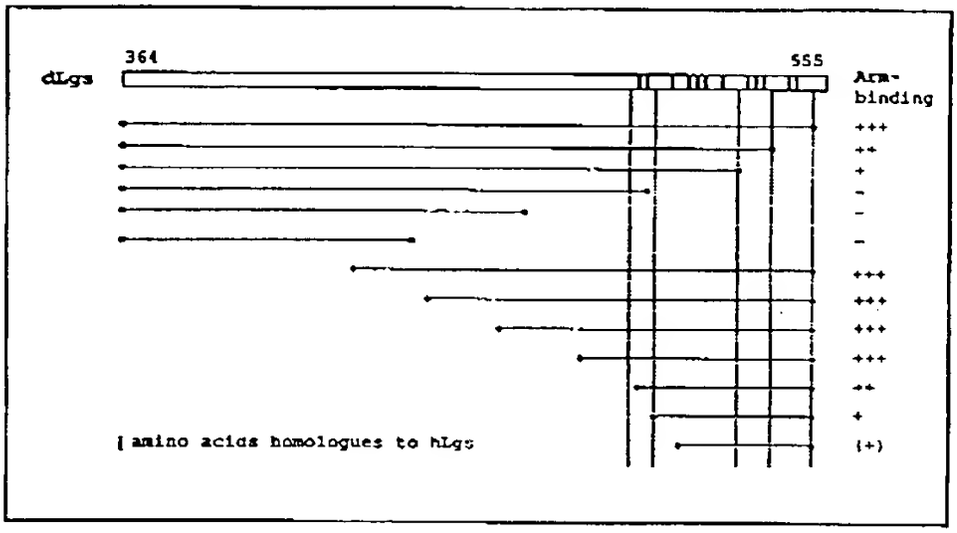

Lgs
GST- 1
2
3
4
5
6
1
1464
1
383
181
555
364
732
549
913
725
1090
1090
1464
IVT ΔArm
220 kD
132
85
50
30
1
2
3
4
5
6
GST

Figure 12B


364
555
dLgs
Arm-binding
+++
++
+
-
-
-
+++
+++
+++
+++
++
+
(+)
amino acids homologues to hLgs

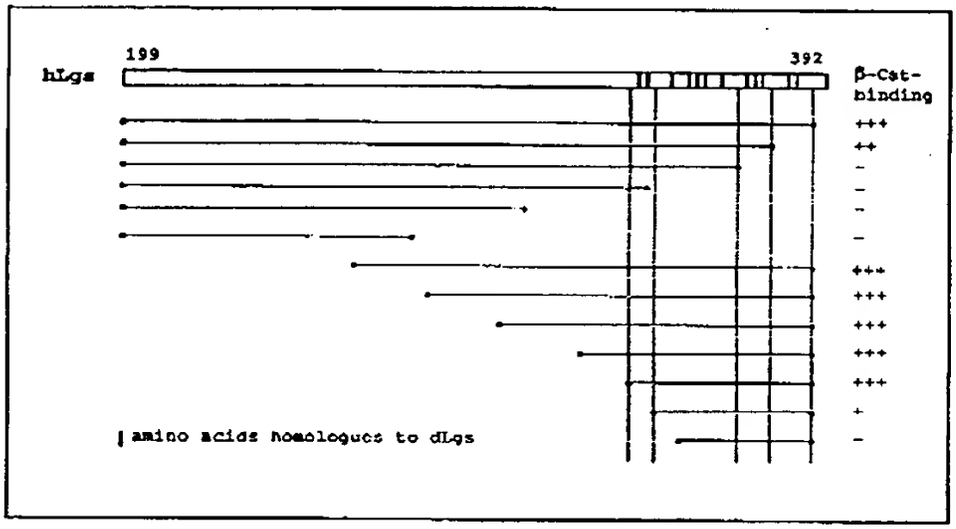

199
392
hLgs
β-Cat-binding
+++
++
-
-
-
-
+++
+++
+++
+++
+++
+
-
amino acids homologues to dLgs

Figure 12C

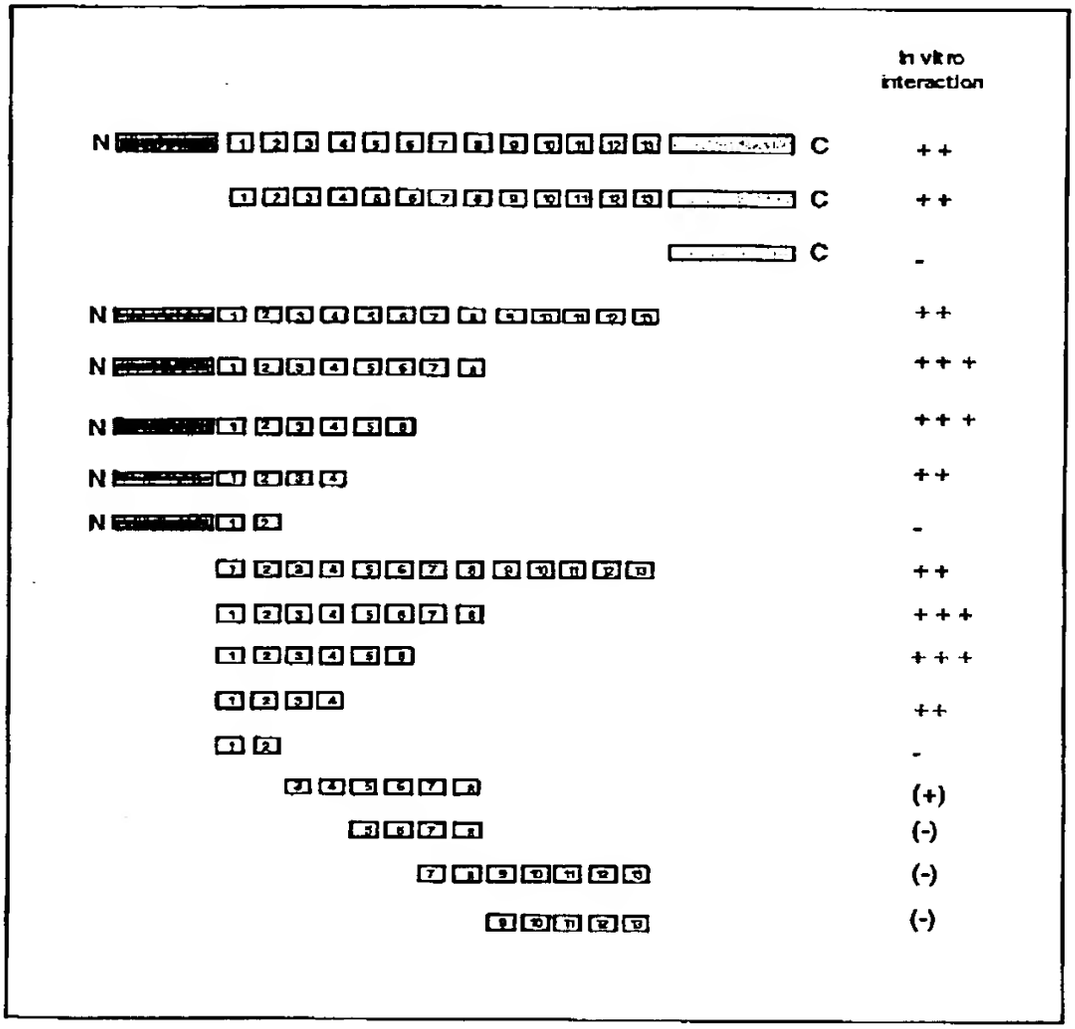
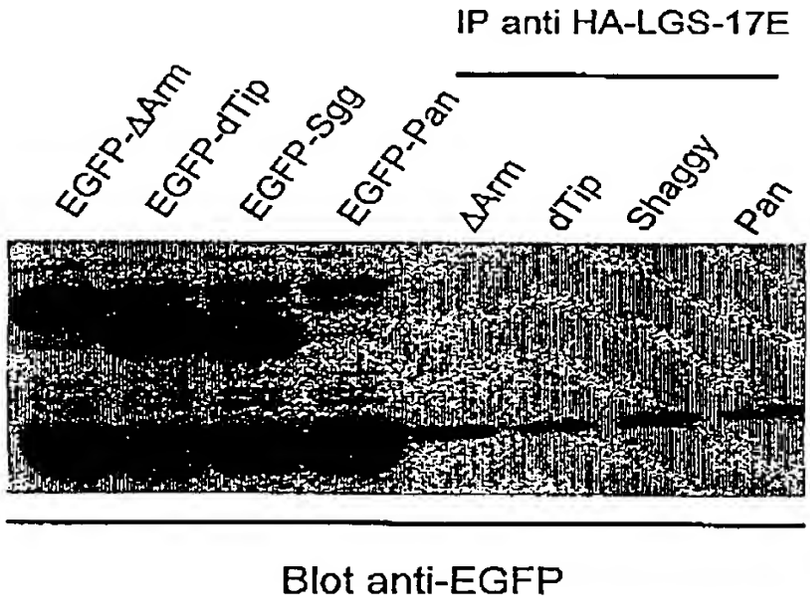


Figure 13

A


IP anti HA-LGS-17E
EGFP-ΔArm
EGFP-dTip
EGFP-Sgg
EGFP-Pan
ΔArm
dTip
Shaggy
Pan
Blot anti-EGFP

B

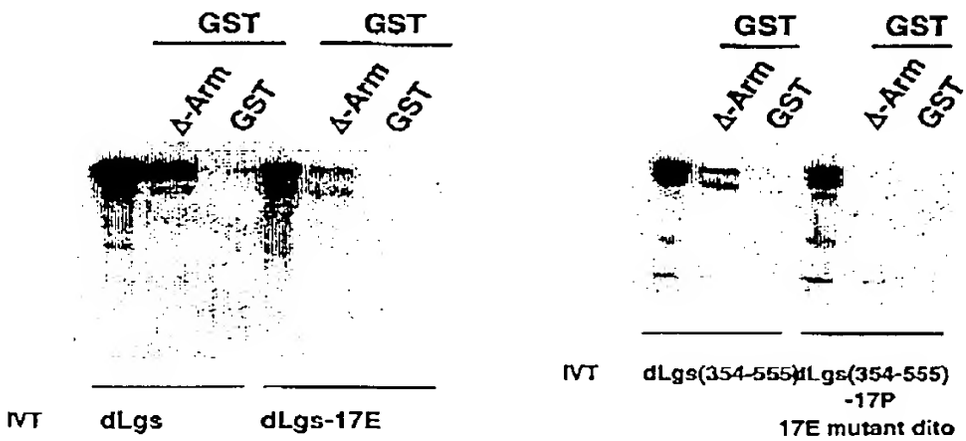
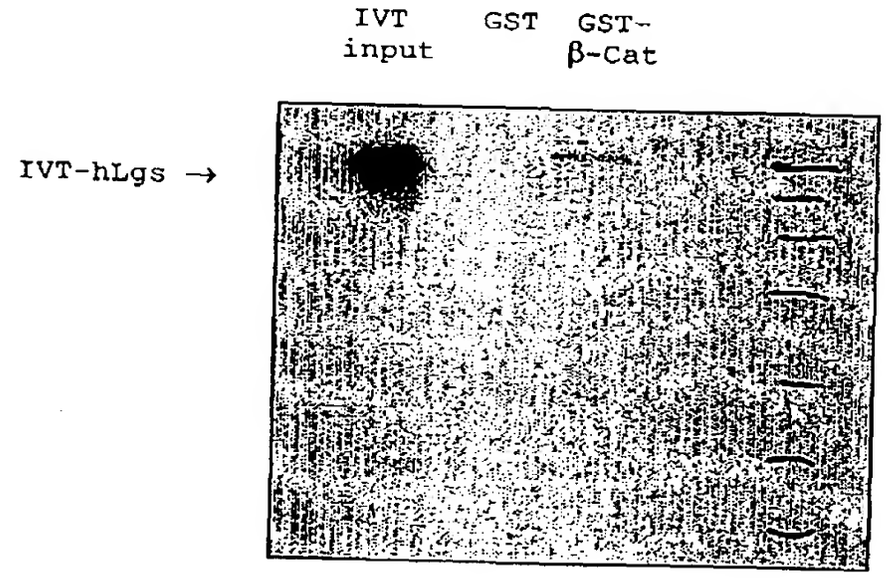

GST
GST
Δ-Arm
GST
Δ-Arm
GST
IVT
dLgs
dLgs-17E
GST
GST
Δ-Arm
GST
Δ-Arm
GST
IVT
dLgs(354-555)
dLgs(354-555)
-17P
17E mutant dito

Figure 13

C


IVT input
GST
GST-β-Cat
IVT-hLgs →

D

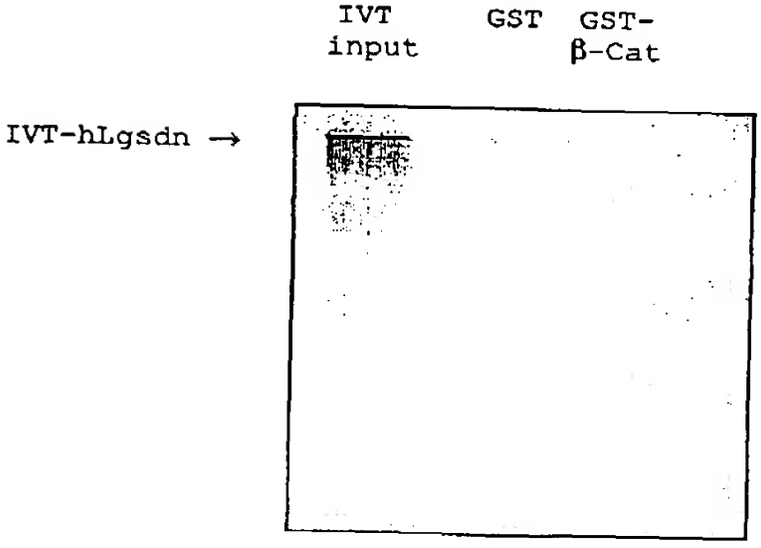
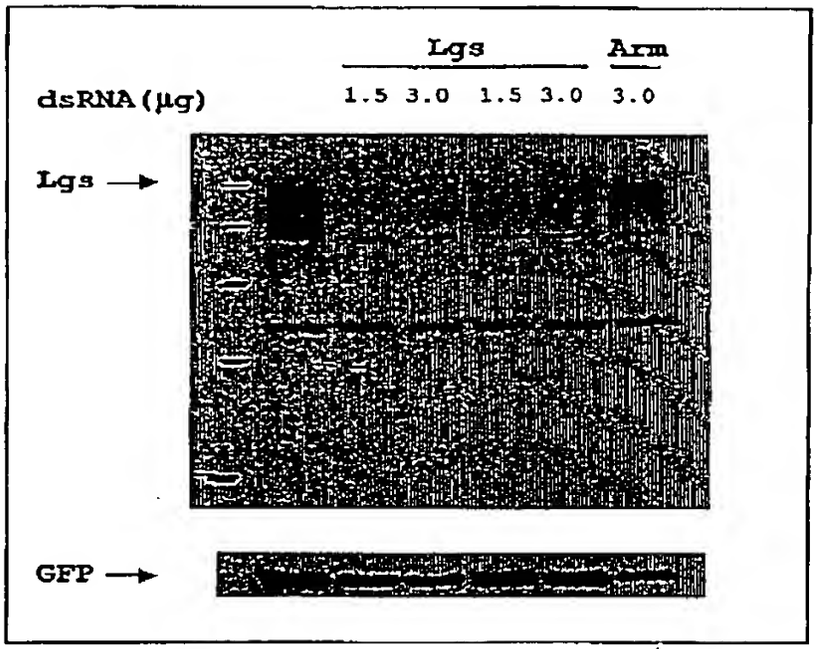
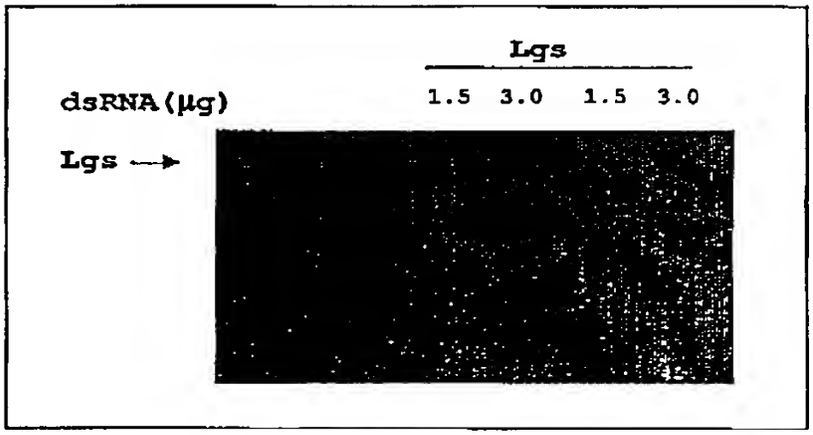

IVT input
GST
GST-β-Cat
IVT-hLgsdn →

Figure 14



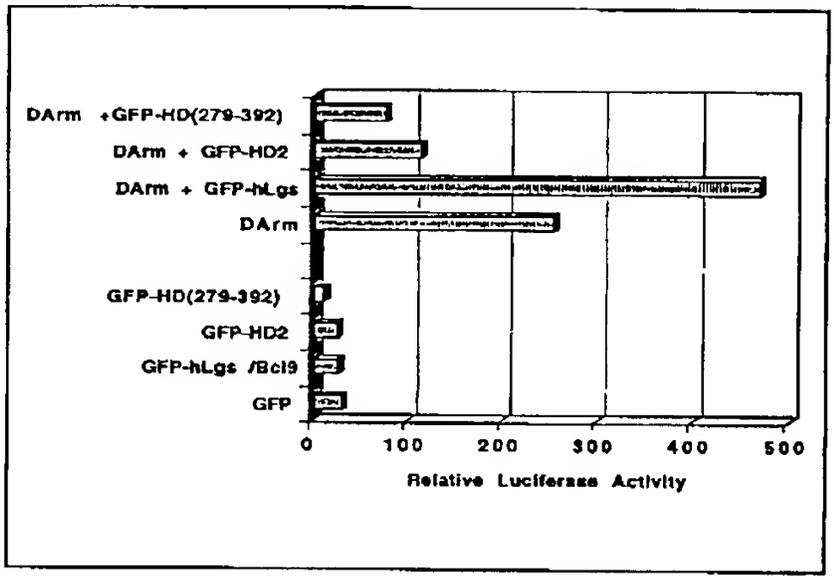
pMT-EGFP (µg) 1.5 1.5 1.5 1.5 1.5 1.5



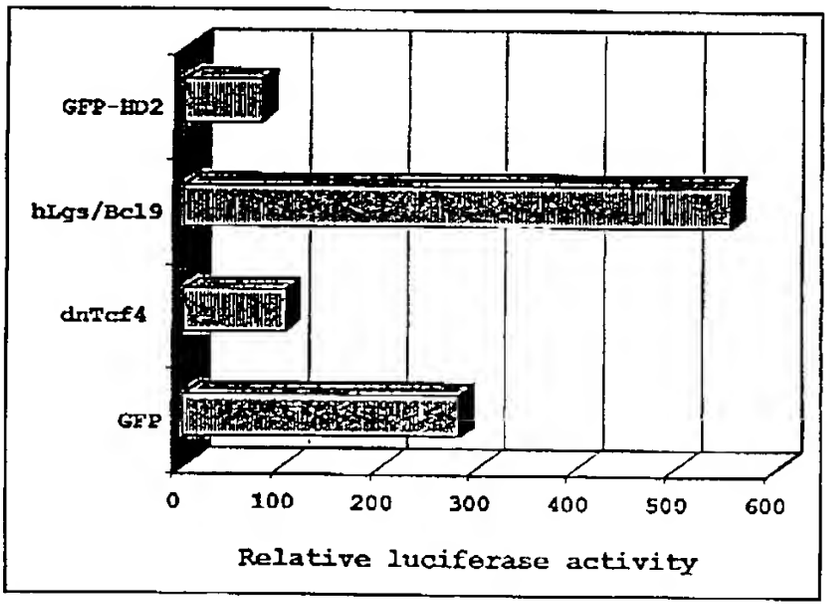
pMT-dLgs (µg) - 2 2 2 2 2

Figure 15

A


DArm +GFP-HD(279-392)
DArm + GFP-HD2
DArm + GFP-hLgs
DArm
GFP-HD(279-392)
GFP-HD2
GFP-hLgs /Bcl9
GFP
0
100
200
300
400
500
Relative Luciferase Activity

B


GFP-HD2
hLgs/Bcl9
dnTcf4
GFP
0
100
200
300
400
500
600
Relative luciferase activity